



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 143390**

**TO: Phillip Gambel**  
**Location: 3e81 / 3c70**  
**Wednesday, February 02, 2005**  
**Art Unit: 1644**  
**Phone: 272-0844**  
**Serial Number: 08 / 485163**

**From: Jan Delaval**  
**Location: Biotech-Chem Library**  
**Rem 1a51**  
**Phone: 272-2504**  
  
**jan.delaval@uspto.gov**

### **Search Notes**

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2005, 21:53:18 ; Search time 10474.2 Seconds  
(without alignments)  
11205.958 Million cell updates/sec

Title: US-08-485-163-4

Perfect score: 2482

Sequence: 1 CAAGCCGAGAGCCCTGGCCAT.....TGAGGAGGACGAGTGGCTC 2482

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_htg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pc: \*  
10: gb\_ro: \*  
11: gb\_sls: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vt: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2482	100.0	2482	6	AR100741 Sequence
2	2482	100.0	2482	6	AR125611 Sequence
3	2482	100.0	2482	6	AR130196 Sequence
4	2482	100.0	2482	6	AR184212 Sequence
5	2482	100.0	2482	6	AR229602 Sequence
6	1795.8	72.3	2009	9	HUMIGCD1
7	1793.4	72.3	2010	9	AF449616
8	1791.8	72.2	2010	9	AF449618
9	1790.2	72.1	2010	9	AF449617
10	1785.4	71.9	56310	2	AC084717 Homo sapi
11	1778	71.6	176237	9	CNS08CBF
12	1775.8	71.5	2010	9	HS250170
13	1692.8	68.2	10785	6	AR367391
14	1641.2	66.1	4694	6	AX088865
15	1641.2	66.1	4694	6	AX478055
16	1637.8	65.9	169802	9	CNS01DT2
17	1627	65.6	3282	6	AR038306
18	1627	65.6	3282	6	AR038320
19	1627	65.6	3282	6	IS58595

c	20	1627	65.6	3282	6	IS58609
c	21	1627	65.6	13254	6	AR038307
c	22	1627	65.6	13254	6	AR038321
c	23	1627	65.6	13254	6	IS58596
c	24	1627	65.6	13254	6	IS58610
c	25	1626.2	65.5	2802	9	HS1G51CP
c	26	1626.2	65.5	4367	6	AX777471
c	27	1626.2	65.5	4723	6	AR161379
c	28	1626.2	65.5	4723	6	AR369972
c	29	1626.2	65.5	4723	6	AX088864
c	30	1626.2	65.5	4723	6	AX478054
c	31	1626.2	65.5	4723	6	BD096606
c	32	1624.8	65.5	4926	6	AR161427
c	33	1624.8	65.5	4926	6	AR370022
c	34	1624.8	65.5	4926	6	BD096656
c	35	1624	65.4	8690	6	BD021874
c	36	1622.4	65.4	8691	6	BD021861
c	37	1621.6	65.3	8614	6	AR176314
c	38	1621.6	65.3	8614	6	AR216773
c	39	1621.6	65.3	8614	6	BD131045
c	40	1621.2	65.3	7874	6	BD021875
c	41	1617.2	65.2	2028	9	HUMIGCD2
c	42	1617.2	65.2	2029	6	AR035227
c	43	1617.2	65.2	2029	6	BD182702
c	44	1617.2	65.2	2399	6	AR264654
c	45	1617.2	65.2	2560	6	AR035228

#### ALIGNMENTS

RESULT 1	AR100741	2482 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR100741	Sequence 3 from patent US 6083478.			
DEFINITION	Sequence 3 from patent US 6083478.				
ACCESSION	AR100741				
VERSION	AR100741.1	GI:12811539			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 2482)				
AUTHORS	Allaway, G.P. and Madden, P.J.				
TITLE	Non-peptidyl moiety-conjugated CD4-gamma2 and CD4-IgG2				
JOURNAL	Immunocombinates, and uses thereof				
FEATURES	Patent: US 6083478-A 3 04-JUN-2000;				
source	Location/Qualifiers				
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	/organism="unknown"				
	/mol_type="unassigned DNA"				
ORIGIN					
Query Match	100.0%; Score 2482; DB 6; Length 2482;				
Best Local Similarity	100.0%; Pred. No. 0;				
Matches 2482; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	CAAGCCGAGAGCCCTGGCCATTTCTGTGGGCTCAGATCCCTAAGCCCTTCTCC	60		
Db	1	CAAGCCGAGAGCCCTGGCCATTTCTGTGGGCTCAGATCCCTAAGCCCTTCTCC	60		
Qy	61	CTGGGAGGAGGACCAATGAAACCGGGAGTCCCTTTAGGCACTTGCTTCTGTGAA	120		
Db	61	CTGGGAGGAGGACCAATGAAACCGGGAGTCCCTTTAGGCACTTGCTTCTGTGAA	120		
Qy	121	CTGGGAGGAGGACCAATGAAACCGGGAGTCCCTTTAGGCACTTGCTTCTGTGAA	180		
Db	121	CTGGGAGGAGGACCAATGAAACCGGGAGTCCCTTTAGGCACTTGCTTCTGTGAA	180		
Qy	181	ACAGTGAATGACCTGTGACGCTTCCGAGGAGGACATCAATTCACATGAGAAAC	240		
Db	181	ACAGTGAATGACCTGTGACGCTTCCGAGGAGGACATCAATTCACATGAGAAAC	240		
Qy	241	TCACACGATTAAGATTCTGGGAATCAGGGCTCTTCTTAATAAGATTCATCCAG	300		

Db 241 TCCAAACAGATAAAGATTCTGGAATCAGGGCTCTTCTTAACTAAAGGTCATCCAAAG 300  
Qy 301 CTGAATGATGCGCTGACTCAAGAAAGACCTTTGGGACCAAGGAACCTTCCCTCATC 360  
Db 301 CTGAATGATGCGCTGACTCAAGAAAGACCTTTGGGACCAAGGAACCTTCCCTCATC 360  
Qy 361 ATCAAGATCTTAAAGATAGAAAGCTCAGATACATTAATCTGTGAAGTGAAGCAAGAG 420  
Db 361 ATCAAGATCTTAAAGATAGAAAGCTCAGATACATTAATCTGTGAAGTGAAGCAAGAG 420  
Qy 421 GAGAGGCTGCAATGCTAGTGTGGATGACTGCAACTTGACACCACCTGCTTAC 480  
Db 421 GAGAGGCTGCAATGCTAGTGTGGATGACTGCAACTTGACACCACCTGCTTAC 480  
Qy 481 GGGGAGGCTGACCTGACCTTGGAGAGCCCTGTGTAGTACCCCTGATGCAATGT 540  
Db 481 GGGGAGGCTGACCTGACCTTGGAGAGCCCTGTGTAGTACCCCTGATGCAATGT 540  
Qy 541 AGGAGTCCAAAGGGGTAAACATACAGGGGGGAAAGACCTCTCGGTCTCAGCTGAG 600  
Db 541 AGGAGTCCAAAGGGGTAAACATACAGGGGGGAAAGACCTCTCGGTCTCAGCTGAG 600  
Qy 601 CTCAGATATAGGCACTGCAATGCACTGTCTTGCAAGAACCAAGAAAGTGAAGTTC 660  
Db 601 CTCAGATATAGGCACTGCAATGCACTGTCTTGCAAGAACCAAGAAAGTGAAGTTC 660  
Qy 661 AAAATAGACATGATGCTAGTCTAGCTTTGACCTCAACAAAGGGCCATGGGTCTTCCCTG 720  
Db 661 AAAATAGACATGATGCTAGTCTAGCTTTGACCTCAACAAAGGGCCATGGGTCTTCCCTG 720  
Qy 721 GCGGCTGCTCCAGAGAGCACTCCAGAGAGCAAGCCGCTGGCTGCTGCTGCAAGAG 780  
Db 721 GCGGCTGCTCCAGAGAGCACTCCAGAGAGCAAGCCGCTGGCTGCTGCTGCAAGAG 780  
Qy 781 TACTTCCCGGAAACCGGTGACGCTGTCTGGAATCTCAGGCGCTGACACAGGGGTGAC 840  
Db 781 TACTTCCCGGAAACCGGTGACGCTGTCTGGAATCTCAGGCGCTGACACAGGGGTGAC 840  
Qy 841 ACCTTCCAGCTGTCTTACAGATCCCAAGAGCTCTTACCTCCCAAGAGTGTGTGAC 900  
Db 841 ACCTTCCAGCTGTCTTACAGATCCCAAGAGCTCTTACCTCCCAAGAGTGTGTGAC 900  
Qy 901 CCTCTCAGCACTTCCGACCCCAAGCTTCACTGCAAGTATGCAAGCCCAAGCAAC 960  
Db 901 CCTCTCAGCACTTCCGACCCCAAGCTTCACTGCAAGTATGCAAGCCCAAGCAAC 960  
Qy 961 ACCAAGGTGACAAAGACATGTTGTGAGAGCCAGCTCAGGAGGAGGTGTCTGAG 1020  
Db 961 ACCAAGGTGACAAAGACATGTTGTGAGAGCCAGCTCAGGAGGAGGTGTCTGAG 1020  
Qy 1021 AGCCAGGCTCAGCCCTCTGCTGAGAGCAACCCGCGCTGTGACCCCAAGCCAGGAG 1080  
Db 1021 AGCCAGGCTCAGCCCTCTGCTGAGAGCAACCCGCGCTGTGACCCCAAGCCAGGAG 1080  
Qy 1081 CAAGGAGGCTTCTGCTCTCTCAGCCGAGGCTCTGCGCGCCCACTCATGCTCAG 1140  
Db 1081 CAAGGAGGCTTCTGCTCTCTCAGCCGAGGCTCTGCGCGCCCACTCATGCTCAG 1140  
Qy 1141 GGAAGGCTCTTCTGCTTTTCCACAGGCTCCAGGAGCAAGGCTGAGTCCCTTA 1200  
Db 1141 GGAAGGCTCTTCTGCTTTTCCACAGGCTCCAGGAGCAAGGCTGAGTCCCTTA 1200  
Qy 1201 CCCAGGCTCTTCAACAGAGGAGGTGCTTGGCTCAGACTGCAAGGCAATATCC 1260  
Db 1201 CCCAGGCTCTTCAACAGAGGAGGTGCTTGGCTCAGACTGCAAGGCAATATCC 1260  
Qy 1261 GGAAGGAGCTCTGCTGCTTAAAGCCGACCCCAAGGCAAGTGTCTCTCCCTGAGC 1320  
Db 1261 GGAAGGAGCTCTGCTGCTTAAAGCCGACCCCAAGGCAAGTGTCTCTCCCTGAGC 1320  
Qy 1321 TCGGACACTTCTCTCTCCAGATCCAGATCTCCCAATCTTCTCTGCAAGGCGCA 1380  
Db 1321 TCGGACACTTCTCTCTCCAGATCCAGATCTCCCAATCTTCTCTGCAAGGCGCA 1380  
Db 1381 AATGTTGTGAGTGGCCACCGGTCCAGTAAAGCCAGGCTCGGCTCCAGCT 1440  
Qy 1381 AATGTTGTGAGTGGCCACCGGTCCAGTAAAGCCAGGCTCGGCTCCAGCT 1440  
Db 1441 CAAGGCGGAGCAGGTGCTTAAAGTACCTGCAATCCAGGAGCAAGGCTGAGTGTCT 1500  
Qy 1441 CAAGGCGGAGCAGGTGCTTAAAGTACCTGCAATCCAGGAGCAAGGCTGAGTGTCT 1500  
Db 1441 CAAGGCGGAGCAGGTGCTTAAAGTACCTGCAATCCAGGAGCAAGGCTGAGTGTCT 1500  
Qy 1501 GACACGTCCACCTTCACTCTTCTTCTGACACCACTGTGTGAGGAGCCGTGCTTCTC 1560  
Db 1501 GACACGTCCACCTTCACTCTTCTTCTGACACCACTGTGTGAGGAGCCGTGCTTCTC 1560  
Qy 1561 TTCCCTCCAAACCCCAAGGACACCTCATATATCTCCGAGACCTGTAGTCAAGTGTG 1620  
Db 1561 TTCCCTCCAAACCCCAAGGACACCTCATATATCTCCGAGACCTGTAGTCAAGTGTG 1620  
Qy 1621 GTGTGAGCCTGAGCCAGAGACCCCGAGGTCCAGTTCACTGTGACGAGCGGTG 1680  
Db 1621 GTGTGAGCCTGAGCCAGAGACCCCGAGGTCCAGTTCACTGTGACGAGCGGTG 1680  
Qy 1681 GAGGTGATATATGCAAGAACCAAGGAGGAGGAGGAGGAGTCAAGTGTGAG 1740  
Db 1681 GAGGTGATATATGCAAGAACCAAGGAGGAGGAGGAGGAGTCAAGTGTGAG 1740  
Qy 1741 GTGAGGCTCTCAGCTGTGTGCAACAGGACTGGAACGGCAAGAGTCAAGTGTGAG 1800  
Db 1741 GTGAGGCTCTCAGCTGTGTGCAACAGGACTGGAACGGCAAGAGTCAAGTGTGAG 1800  
Qy 1801 GTCTCCAAAGAGGCTCCAGGCCCCATGAGAAACCATCTTCCAAACCAAGGTGAG 1860  
Db 1801 GTCTCCAAAGAGGCTCCAGGCCCCATGAGAAACCATCTTCCAAACCAAGGTGAG 1860  
Qy 1861 ACCGCGGGGTATGAGGGGCAATGACAGAGGCGGCTGAGCCCTGCTGCTGAG 1920  
Db 1861 ACCGCGGGGTATGAGGGGCAATGACAGAGGCGGCTGAGCCCTGCTGCTGAG 1920  
Qy 1921 AGTACCGCTGTGCAACCTCTGCTTCAAGGGAGCCCGAGAACCAAGGTGAC 1980  
Db 1921 AGTACCGCTGTGCAACCTCTGCTTCAAGGGAGCCCGAGAACCAAGGTGAC 1980  
Qy 1981 CTTGCCCCATCCCGGAGGAGATGACCAAGAACCAAGTCAAGCTGAGCTGCTGCA 2040  
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Qy 2101 CTACAAAGACACCTCCCAATGCTGACCTCGACGCTCTTCTTCTTACAGCAAGCT 2160  
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Qy 2161 CACGTTGAGCAAGAGCAGTGTGAGAGGAGGAGAACTTCTTCAATGCTCCGTAATGA 2220  
Db 2161 CACGTTGAGCAAGAGCAGTGTGAGAGGAGGAGAACTTCTTCAATGCTCCGTAATGA 2220  
Qy 2221 GGTCTTGAACAACAATACAGAGAGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTG 2280  
Db 2221 GGTCTTGAACAACAATACAGAGAGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTG 2280  
Qy 2281 ACCGCGGAGAGCCCGGCTCCCAAGGCTCTCGGGGTGAGTGAAGTGTGCAAGTGA 2340  
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Db 2401 GCCCTGAGAGCTGTGATGTTCTTTCGTTGAGTCAAGGCTGAGGCTGAGTGTG 2460

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 03:40:26 ; Search time 7912.19 Seconds  
(without alignment) 11430.900 Million cell updates/sec

Title: US-08-485-163-4

Perfect score: 2482  
Sequence: 1 CAAGCCGAGAGCCCTGCGCAT.....TGAGGAGGACGAGTGGGTC 2482

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hic: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gse1: \*  
9: gb\_gse2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	720.2	29.0	1231	3	CR592363 full-length
2	713.2	28.7	1224	3	CR625121 full-length
3	688.6	27.7	1158	3	CR623267 full-length
4	674.6	27.2	1194	3	CR603811 full-length
5	672.6	27.1	1060	3	CR602446 full-length
6	668.4	26.9	788	5	BX429840 full-length
7	665.6	26.8	1012	3	CR595292 full-length
8	659.4	26.6	805	5	BX429839 full-length
9	655.4	26.4	932	5	BX438745 full-length
10	645.4	26.0	783	6	CD609192 5606931J
11	644.4	26.0	904	5	BX351808 full-length
12	643.6	25.9	1113	3	CR611470 full-length
13	643.6	25.9	812	5	BX429780 full-length
14	643.2	25.9	816	4	BX429780 full-length
15	642.8	25.9	816	4	BX429780 full-length
16	640.6	25.8	1097	3	CR590214 full-length
17	640.6	25.8	1097	3	CR590214 full-length
18	635.8	25.6	785	5	BX429838 full-length
19	633.2	25.6	1287	3	CR611016 full-length
20	634.6	25.6	902	3	CR608756 full-length
21	634.6	25.6	918	3	CR597050 full-length
22	634.6	25.6	975	3	CR608814 full-length
23	634.6	25.6	1091	3	CR604840 full-length
24	634.6	25.6	1091	3	CR611575 full-length

25	633.6	25.5	1089	3	CR599517 full-length
26	633.6	25.5	1090	3	CR594433 full-length
27	633.4	25.5	801	4	BI822118 603039813
28	632.6	25.5	1089	3	CR604209 full-length
29	632	25.5	822	5	BX457159 full-length
30	631.2	25.4	1136	3	CR598462 full-length
31	629.6	25.4	1086	3	CR603347 full-length
32	629.6	25.4	1086	3	CR603347 full-length
33	629	25.3	840	4	BI838893 603087279
34	628.6	25.3	1057	5	BX417147 full-length
35	625.6	25.2	1224	3	CR609874 full-length
36	624.2	25.1	1142	3	CR598316 full-length
37	623.2	25.1	1078	3	CR602414 full-length
38	622.6	25.1	1039	5	BX355903 full-length
39	622.4	25.1	791	4	BI819727 603041415
40	622.4	25.1	845	5	BX367837 full-length
41	620.8	25.0	1120	3	CR619868 full-length
42	620.4	25.0	1022	5	BX385912 full-length
43	619	24.9	760	6	CA447963 full-length
44	618.6	24.9	784	5	BQ112730 full-length
45	616.6	24.8	1068	5	BX359678 full-length

#### ALIGNMENTS

RESULT 1	CR592363	1231 bp	mRNA	linear	HTC 21-JUL-2004
LOCUS	CR592363				
DEFINITION	full-length cDNA clone CS0DE006YX04 of Placenta of Homo sapiens (human).				
ACCESSION	CR592363				
VERSION	CR592363.1	GI:50473170			
KEYWORDS	HTC; CNSLT cDNA.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact : Feng Liang Email : fliang@life.techn.com URL : http://fulllength.invitrogen.com/ invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1231)				
REFERENCE	Genoscope.				
AUTHORS	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :				
TITLE	BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr				
JOURNAL	- Web : www.genoscope.cns.fr				
COMMENT	1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.				
FEATURES	Location/Qualifiers				
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ORIGIN					
Query Match	29.0% ; Score 720.2 ; DB 3 ; Length 1231 ;				
Best Local Similarity	87.0% ; Pred. No. 4.1e-167 ;				
Matches	857 ; Conservative 0 ; Mismatches 28 ; Indels 100 ; Gaps 2 ;				
OY	1395 TGCCACGCGCCGAGTGAAGCAGCAGGCGCTCGCCTCAGCTCAAGCGGAGCAGG 1454				
DB	344 TGCCACGATGTGCAAGTGAAGCAGCAGGCGCTCGCCTCAGCTCAAGCGGAGCAGG 403				

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QY 1455 TGCCCTAGAGTAGGCTGATCCAGGACAGGCCCCAGCTGGGTGCTGACAGTCCACTC 1514
Db 404 TGCCCTAGAGTAGGCTGATCCAGGACAGGCCCCAGGCTGCTGACAGTCCGCTC 463
QY 1515 CATCTCTTCTCTGAGACC--ACCTGTGGCAGAGACCGTCACTTCTCTTCCCCCAA 1571
Db 464 CATCTCTTCTCTGAGACC--ACCTGTGGCAGAGACCGTCACTTCTCTTCCCCCAA 523
QY 1572 ACCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAAGTGGGTGGTGGACGT 1631
Db 524 ACCCAAGGATACCTCATGATCTCCCGGACCCCTGAGGTCAAGTGGGTGGTGGACGT 583
QY 1632 GAGCCACGAAAGACCCCGAGGTTCAGTTCACTGTGACGTGACCGCGTGGAGTGCATTA 1691
Db 584 GAGCCACGAAAGACCCCTGAGGTTCAGTTCACTGTGACGTGACCGCGTGGAGTGCATTA 643
QY 1692 TGCCAAAGCAAAAGCCGAGAGAGACAGTCAACAGACGTTCCGTGTGTGCTGAGGTCT 1751
Db 644 TGCCAAAGCAAAAGCCGAGAGAGACAGTCAACAGACGTTCCGTGTGTGCTGAGGTCT 703
QY 1752 CACCGTGTGACACAGACGTGGTGAAGGAGAGAGTCAAGTGCAGAGTCTCCAA 1811
Db 704 CACCGTGTGACACAGAGCTGGTGAAGGAGAGAGTCAAGTGCAGAGTCTCCAA 763
QY 1812 AGGCTCTCCAGCCCGCATCGAAGAAACCATCTCCAAACCAAGGTGGGACCCGCGGGGT 1871
Db 764 AGGCTCTCCAGCCCGCATCGAAGAAACCATCTCCAAACCAAGGTGGGACCCGCGGGGT 805
QY 1872 ATGAGGGCCACATGAGACAGAGCGGGCTCGGCCCACTCTGCTGGAGTGAACCGCTG 1931
Db 806 ----- 805
QY 1932 TGCCAACTCTGTCCCTACAGGGGAGCCCGGAGAACCAAGTGTACACCTTGCCCCAT 1991
Db 806 -----AGGGCAGCCCGAGAACCAAGTGTACACCTTGCCCCAT 846
QY 1992 CCGGAGAGAGATGACCAAGAACAGGTCAAGCTGACCTGCTGGTCAAAAGCTTCTTACC 2051
Db 847 CCGGAGAGAGATGACCAAGAACAGGTCAAGCTGACCTGCTGGTCAAAAGCTTCTTACC 906
QY 2052 CCAAGACATGCGGTGGAGTGGAGAGCAATGGGACCGGAGAACCACTACAAAGCA 2111
Db 907 CCAAGACATGCGGTGGAGTGGAGAGCAATGGGACCGGAGAACCACTACAAAGCA 966
QY 2112 CACCTCCATGCTGAGACCTCGACCGGCTCTTCTCTTACAGCAAGTTCACCGTGA 2171
Db 967 CACCTCCATGCTGAGACCTCGACCGGCTCTTCTCTTACAGCAAGTTCACCGTGA 1026
QY 2172 AGAGCAGTGGCAGCAGGAGGAAAGTCTTCTCATGCTCCGTGATGATGAGGCTGACCA 2231
Db 1027 AGAGCAGTGGCAGCAGGAGGAAAGTCTTCTCATGCTCCGTGATGATGAGGCTGACCA 1086
QY 2232 ACCACTACACGAGAAAGCTCTCTCTGCTCCGGGTAATGAGTGCACGCGCGGCA 2291
Db 1087 ACCACTACACGAGAAAGCTCTCTCTGCTCCGGGTAATGAGTGCACGCGCGGCA 1146
QY 2292 GCGCCCGTCTCCAGGCTCTGCGGGTGGCGTGAAGATCTTGGACGTAACCCCGTGA 2351
Db 1147 GCGCCCGTCTCCAGGCTCTGCGGGTGGCGGAGATCTTGGACGTAACCCCGTGA 1206
QY 2352 TACTTCCAGGACCCAGCATGAA 2376
Db 1207 TACTTCCAGGACCCAGCATGAA 1231

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RESULT 2
CR625121 1224 bp mRNA linear HTC 21-JUL-2004
LOCUS CR625121
DEFINITION of Homo sapiens (human).
ACCESSION CR625121
VERSION CR625121.1 GI:50505928

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KEYWORDS HTC; CNSLT CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1224)
AUTHORS Li, W. B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/InvitrogenCorporation1600
Faraday Avenue
2 (bases 1 to 1224)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequenage :
JOURNAL BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
source 1..1224
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/mol_type="mRNA"
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Best Local Similarity 86.9%; Pred. No. 2,2e-165;
Matches 850; Conservative 0; Mismatches 28; Indels 100; Gaps 2;
QY 1395 TGCCACCGTGCCAGGTAAAGCCAGCCAGGCTCGGCTTCAGACTCAAGGCGGAGCAG 1454
Db 344 TGCCACCAATGTGAAATTAAGCCAGCCAGGCTCGGCTTCAGACTCAAGGCGGAGCAG 403
QY 1455 TGCCCTAGAGTAGGCTGATCCAGGACAGGCCCCAGCTGGGTGCTGACAGTCCACTTC 1514
Db 404 TGCCCTAGAGTAGGCTGATCCAGGACAGGCCCCAGGCTGGGTGCTGACAGTCCGCTC 463
QY 1515 CATCTCTTCTCTGAGACC--ACCTGTGGCAGAGACCGTCACTTCTCTTCCCCCAA 1571
Db 464 CATCTCTTCTCTGAGACC--ACCTGTGGCAGAGACCGTCACTTCTCTTCCCCCAA 523
QY 1572 ACCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAAGTGGGTGGTGGACGT 1631
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QY 1632 GAGCCACGAAAGACCCCGAGGTTCAGTTCAACTGTGACGTGACCGCGTGGAGTGCATTA 1691
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QY 1872 ATGAGGGCCACATGAGACAGAGCGGGCTCGGCCCACTCTGCTGGAGTGAACCGCTG 1931
Db 806 ----- 805

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Title: US-08-485-163-4  
Perfect score: 2482  
Sequence: 1 CAAGCCGAGAGCCCTGCGCAT.....TGAGGAGAGCAGAGTGGGTC 2482

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues  
Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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5	2482	100.0	2482	10	ABBS5721
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7	2472.4	99.6	2482	2	AAQ57751
8	2261.6	91.1	2488	2	AAQ27831
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32	1624.8	65.5	4926	2	AAV39291
33	1624.8	65.5	4926	2	AAZ22045
34	1624.6	65.5	3223	12	ADN61720
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40	1621.6	65.3	8614	6	AAH43776
41	1619.8	65.3	9201	2	AAQ55003
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43	1618	65.2	7874	2	AAV18695
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## ALIGNMENTS

RESULT 1	AAQ28089	AAQ28089 standard; cDNA; 2482 BP.
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DT	25-MAR-2003 (revised)	
DT	06-FEB-1993 (first entry)	
DT	06-FEB-1993 (first entry)	
XX	Encodes CD4-IgG2 chimeric heavy chain.	
XX	homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery;	
KW	chimeric; increased serum half life; HIV infection; AIDS; ss.	
OS	Homo sapiens.	
OS	Chimeric.	
XX		
XX	Key	Location/Qualifiers
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FT	CDS	1528..1854
FT	CDS	/*tag= c
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FT	CDS	/*tag= d
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XX	10-FEB-1992;	92WO-US001143.
XX	08-FEB-1991;	91US-00653684.
XX	(PROG-) PROGENICS PHARM INC.	
PA		

XX Beaudry GA, Maddon PJ;  
XX WPI: 1992-300034/36.  
XX P-PSDB: AAR26783.  
XX CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for  
XX treatment, prevention and diagnosis of HIV infection.  
XX Claim 13; Fig 4; 90pp; English.  
XX  
XX This sequence encodes a CD4-gamma2 chimeric heavy chain homodimer. Human  
XX CD4 cDNA was excised from plasmid pSP614 as an EcoRI/StuI 0.7 kb  
XX fragment, and cloned into M13mp18 forming M13mp18(CD4). This was  
XX linearised with PstI, and the SacII(Flush)/PstI fragment from pBR gamma2  
XX containing human gamma2 heavy chain (CH1 exon) isolated and ligated to  
XX the M13mp18(CD4) vector. Resulting recombinants were then screened by  
XX restriction analysis for the presence of both CD4 and CH1 which occur in  
XX tandem CD4(EcoRI/StuI)-CH1(SacI/Flush)/PstI. Site directed mutagenesis  
XX was performed to juxtapose the CD4 and CH1 heavy chain sequences in  
XX frame. The resulting chimeric DNA molecule encodes a protein containing  
XX the V1V2 domains of CD4 fused to the CH1 domain of heavy chain. Plaques  
XX containing the chimeric gene with the correct sequence were then grown in  
XX TGI cells and RT DNA isolated from the cells. (Updated on 25-MAR-2003 to  
XX correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)  
XX  
XX Sequence 2482 BP; 559 A; 812 C; 676 G; 435 T; 0 U; 0 Other;

Query Match 100.0%; Score 2482; DB 2; Length 2482;  
Blast Local Similarity 100.0%; Pred. No. 0;  
Matches 2482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 09:02:41 ; Search time 1340.46 Seconds  
(without alignments)

10639.123 Million cell updates/sec

Title: US-08-485-163-4

Perfect score: 2482

Sequence: 1 CAAGCCAGAGAGCCCTGCGCAT.....TGAGGAGAGAGAGTGGGTC 2482

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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6	1641.2	66.1	4694	US-09-948-939-41	Sequence 41, Appl1
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12	1627	65.6	13254	US-10-016-986-170	Sequence 170, App

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44	1454.8	58.6	2071	15	US-10-216-484-116	Sequence 116, App
45	1454.8	58.6	2071	15	US-10-384-933-116	Sequence 116, App

#### ALIGNMENTS

RESULT 1

US-08-485-163-4

Sequence 4, Application US/08485163

Publication No. US20020098191A1

GENERAL INFORMATION:

APPLICANT: Beauty, Gary A.

APPLICANT: Maddon, Paul J.

TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESS: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,163

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 2482 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-08-485-163-4

Query Match 100.0%; Score 2482; DB 8; Length 2482;  
Bseq Local Similarity 100.0%; Pred. No. 0;  
Matches 2482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 03:49:56 ; Search time 211.903 Seconds  
(without alignments)  
8325.401 Million cell updates/sec

Title: US-08-485-163-4

Perfect score: 2482

Sequence: 1 CAAGCCGAGAGCCCTGCGCAT.....TGAGGAGAGCAGAGTGCGTC 2482

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	2482	100.0	2482	US-08-379-516-3	Sequence 3, Appl1
3	2482	100.0	2482	US-09-329-916-3	Sequence 3, Appl1
4	2482	100.0	2482	US-08-485-372A-3	Sequence 3, Appl1
5	2482	100.0	2482	US-09-409-006A-3	Sequence 3, Appl1
6	2482	100.0	2482	US-08-484-681-3	Sequence 3, Appl1
7	2482	100.0	2482	US-09-766-995-3	Sequence 3, Appl1
8	2482	100.0	2482	PCT-US93-07422-3	Sequence 3, Appl1
9	1692.8	68.2	10785	US-08-444-644-27	Sequence 27, Appl1
10	1627	65.6	3282	US-08-232-246A-27	Sequence 154, App
11	1627	65.6	3282	US-08-276-852-154	Sequence 154, App
12	1627	65.6	3282	US-08-276-852-159	Sequence 154, App
13	1627	65.6	3282	US-08-899-575-154	Sequence 154, App
14	1627	65.6	3282	US-08-899-575-159	Sequence 154, App
15	1627	65.6	3282	US-08-899-575-154	Sequence 154, App
16	1627	65.6	3282	US-08-899-575-159	Sequence 154, App
17	1627	65.6	3282	PCT-US95-08743-154	Sequence 154, App
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23	1627	65.6	13254	US-08-899-575-156	Sequence 156, App
24	1627	65.6	13254	US-08-899-575-170	Sequence 170, App
25	1627	65.6	13254	PCT-US95-08743-156	Sequence 156, App
26	1627	65.6	13254	PCT-US95-08743-170	Sequence 170, App
27	1626.2	65.5	4723	US-09-042-353-370	Sequence 370, App

28	1626.2	65.5	4723	3	US-08-758-417A-218	Sequence 218, App
29	1624.8	65.5	4926	3	US-09-042-353-418	Sequence 418, App
30	1624.8	65.5	4926	3	US-08-758-417A-268	Sequence 268, App
31	1621.6	65.3	8614	3	US-09-247-352-5	Sequence 5, Appl
32	1621.6	65.3	8614	3	US-09-466-635-5	Sequence 5, Appl
33	1617.2	65.2	2029	2	US-07-916-098A-43	Sequence 43, Appl
34	1617.2	65.2	2399	4	US-08-070-116A-1	Sequence 1, Appl
35	1617.2	65.2	2399	4	US-08-557-050-1	Sequence 1, Appl
36	1617.2	65.2	2560	2	US-07-916-098A-44	Sequence 44, Appl
37	1601.4	64.5	10844	3	US-08-444-644-41	Sequence 41, Appl
38	1601.4	64.5	10844	3	US-08-232-246A-41	Sequence 41, Appl
39	1581.8	63.7	1999	4	US-09-472-087-54	Sequence 54, Appl
40	1574.6	63.4	2770	4	US-09-227-595-29	Sequence 29, Appl
41	1574.6	63.4	2770	4	US-08-595-590B-29	Sequence 29, Appl
42	1573	63.4	2009	1	US-08-109-106-5	Sequence 5, Appl
43	1570	63.3	11528	3	US-08-444-644-18	Sequence 18, Appl
44	1570	63.3	11528	3	US-08-232-246A-18	Sequence 18, Appl
45	1495.4	60.2	1980	1	US-08-109-106-4	Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-08-477-460B-3  
Sequence 3, Application US/08477460B  
Patent No. 6034223  
GENERAL INFORMATION:  
APPLICANT: Progenics Pharmaceuticals, Inc.  
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08477,460B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/927,931  
FILING DATE: 07-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPM/AM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 977-9809  
TELEX: 422523 COOP UT  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2482 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: Lymphocyte  
US-08-477-460B-3  
Query Match 100.0%; Score 2482; DB 3; Length 2482;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6  
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Title: US-08-485-163-6

Perfect score: 1149

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Searched: 4526729 seqs, 2364489745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
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2: gb\_hcg: \*  
3: gb\_in: \*  
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11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_va: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	1149	100.0	1149	6	AR229603 Sequence
6	696.8	60.6	2482	6	AR100741 Sequence
7	696.8	60.6	2482	6	AR125611 Sequence
8	696.8	60.6	2482	6	AR130196 Sequence
9	696.8	60.6	2482	6	AR184212 Sequence
10	696.8	60.6	2482	6	AR229602 Sequence
11	687	59.8	1742	6	AR380468 Sequence
12	687	59.8	1742	6	AX287109 Sequence
13	687	59.8	1742	9	HUMACT4
14	687	59.8	1742	9	HUMACT4A
15	687	59.8	1796	6	AR100740 Sequence
16	687	59.8	1796	6	AR125610 Sequence
17	687	59.8	1796	6	AR130195 Sequence
18	687	59.8	1796	6	AR184211 Sequence
19	687	59.8	1796	6	AR229601 Sequence

20	685.4	59.7	1273	6	106223 Sequence 1
21	685.4	59.7	1742	6	AR104143 Sequence
22	685.4	59.7	1742	6	108673 Sequence 2
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24	685.4	59.7	1742	6	AR448985 Sequence
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26	683.8	59.5	1273	6	107147 Sequence 1
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29	683.8	59.5	1416	6	109301 Sequence 1
30	683.8	59.5	1416	6	127613 Sequence 2
31	683.8	59.5	1416	6	AR489592 Sequence
32	683.8	59.5	1742	6	107208 Sequence 4
33	664	57.8	1213	6	AR363716 Sequence
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35	657	57.2	1304	6	108115 Sequence 3
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37	655.4	57.0	1304	6	AR166802 Sequence
38	655.4	57.0	1537	6	C0722428 Sequence
39	655.4	57.0	2589	6	AR392157 Sequence
40	655.4	57.0	3084	6	BC025782 Homo sapi
41	653.8	56.9	3064	6	109237 Sequence 1
42	652.4	56.8	719	6	AR067944 Sequence
43	652.4	56.8	719	6	AR166803 Sequence
44	652.2	56.8	5566	6	109269 Sequence 36
45	652.2	56.8	6149	6	109252 Sequence 19

#### ALIGNMENTS

RESULT 1  
LOCUS AR100742 1149 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 5 from patent US 6083478.  
ACCESSION AR100742  
VERSION AR100742.1 GI:12811540  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 1149)  
AUTHORS Allaway,G.P. and Madden,P.J.  
TITLE Non-peptidyl moiety-conjugated CD4-gamma2 and CD4-IgG2  
Immunocombinates, and uses thereof  
JOURNAL Patent: US 6083478-A 5 04-JUN-2000;  
FEATURES  
source location/Qualifiers  
1..1149  
/organism="Unknown"  
/mol\_type="unassigned DNA"

#### ORIGIN

Query Match 100.0%; Score 1149; DB 6; Length 1149;  
Best Local Similarity 100.0%; Pred. No. 3.2e-292; Indels 0; Gaps 0;  
Matches 1149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAAGCCGAGACCCCTGCGCATTTCTGTGGCTCAGGTCCTACTGTCAGCCCTTCTCC 60  
DB 1 CAAGCCGAGACCCCTGCGCATTTCTGTGGCTCAGGTCCTACTGTCAGCCCTTCTCC 60  
QY 61 CTCGGCAAGGCGCACATTAACCGGGAGTCCCTTTTAAAGCACTTGCTGTGCA 120  
DB 61 CTCGGCAAGGCGCACATTAACCGGGAGTCCCTTTTAAAGCACTTGCTGTGCA 120  
QY 121 CTGGGCTCTCTCCGACGACCTCAGGGAAGAAAGTGCTGGCAAAAAGGGGAT 180  
DB 121 CTGGGCTCTCTCCGACGACCTCAGGGAAGAAAGTGCTGGCAAAAAGGGGAT 180  
QY 181 ACAGTGAATGACCTGTACAGCTTCCGAGAAAGACATCAATTCCTACTGAAAAAC 240  
DB 181 ACAGTGAATGACCTGTACAGCTTCCGAGAAAGACATCAATTCCTACTGAAAAAC 240  
QY 241 TCACAACGATTAAGATTCTGGGAAATCAGGGCTCTCTTAATCAAGATTCATCCAG 300

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Db      241  TCCAAACAGATAAAGATTCTGGGAAATCAGGGCTCTCTTAACTAAAGGTCATCAAG 300
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Db      301  CTGAATGATCGCGCTGACTCAAGAGAAAGCTTTGGGACCAAGAACTTCCCTGATC 360
Qy      361  ATCAAGATCTTAAAGATAGAAAGCTCAGATTAATCTGTGTGAAGTGAAGACAGAG 420
Db      361  ATCAAGATCTTAAAGATAGAAAGCTCAGATTAATCTGTGTGAAGTGAAGACAGAG 420
Qy      421  GAGAGGTGCAATTGCTAGTGTGGATTAAGTCCAACTTGAACCCACCTGCTTAC 480
Db      421  GAGAGGTGCAATTGCTAGTGTGGATTAAGTCCAACTTGAACCCACCTGCTTAC 480
Qy      481  GGGGAGGCTGACCTGACCTTGAAGAGCCCTGGTAGTACCCCTGAGTCATGT 540
Db      481  GGGGAGGCTGACCTGACCTTGAAGAGCCCTGGTAGTACCCCTGAGTCATGT 540
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Qy      601  CTCAGAGTATGGGCACTGAGCATGCACTGCTTTCAGAAACCAAGAAAGTGAAGTTC 660
Db      601  CTCAGAGTATGGGCACTGAGCATGCACTGCTTTCAGAAACCAAGAAAGTGAAGTTC 660
Qy      661  AAAATAGACATGCTGCTGCTAGCTTTCACTGAGCTGACCATGCTTCACTTCCG 720
Db      661  AAAATAGACATGCTGCTGCTAGCTTTCACTGAGCTGACCATGCTTCACTTCCG 720
Qy      721  CCATCTGATGAGCAGTTGAAATCTGAACTGCTCTGTGTGTGCTGCTGATTAATCTTC 780
Db      721  CCATCTGATGAGCAGTTGAAATCTGAACTGCTCTGTGTGTGCTGCTGATTAATCTTC 780
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Db      781  TATCCCAAGAGGCGCAAAAGTCACTGGAAGGTGATTAACGCTTCAATGGGTAACTCC 840
Qy      841  CAGAGAGTGTCAAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAG 900
Db      841  CAGAGAGTGTCAAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAG 900
Qy      901  ACAGTGAAGCAAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAG 960
Db      901  ACAGTGAAGCAAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAG 960
Qy      961  GGCTGAGCTGCGCTGCAAAAGAGCTTCAAGAGGAGAGTGTAGAGGAGAGAGTGC 1020
Db      961  GGCTGAGCTGCGCTGCAAAAGAGCTTCAAGAGGAGAGTGTAGAGGAGAGAGTGC 1020
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Db      1021  CCCCACGTCCTCAGTTCAGAGCTGACCCCTCCCACTCTTGGCTCTGACCTTTT 1080
Qy      1081  TCCAAGAGGAGCAGTACCTTATGCGGCTCTCAAGCTCATCTTCACTCAACCCCTC 1140
Db      1081  TCCAAGAGGAGCAGTACCTTATGCGGCTCTCAAGCTCATCTTCACTCAACCCCTC 1140
Qy      1141  CTCTCTCTT 1149
Db      1141  CTCTCTCTT 1149

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RESULT 2
ARI25612      1149 bp      DNA      linear      PAT 16-MAY-2001
LOCUS        Sequence 5 from patent US 6177549.
ACCESSION   ARI25612
VERSION     ARI25612.1  GI:14111674
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.

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REFERENCE    Unclassified.
AUTHORS      1 (bases 1 to 1149)
TITLE        Maddon, P.J. and Allaway, G.P.
JOURNAL      Non-peptidyl moiety-conjugated CD4-gamma2 and CD4-IgG2
FEATURES     immunoconjugates, and uses thereof
SOURCE       Patent: US 6177549-A 5 23-JAN-2001;
              Location/Qualifiers
              1. 1149
              /organism="unknown"
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ORIGIN
Query Match 100.0%; Score 1149; DB 6; Length 1149;
Best Local Similarity 100.0%; Pred. No. 3.2e-292;
Matches 1149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CAAAGCCAGAGCCCTGCAATTTCTGTGGGCTCAGGTCCCTAAGTCTCAAGCCCTTCTCC 60
Db      1  CAAAGCCAGAGCCCTGCAATTTCTGTGGGCTCAGGTCCCTAAGTCTCAAGCCCTTCTCC 60
Qy      61  CTGGGCAAGGCACAATGAACCGGGAGTCCCTTTTAGGCACTTGTGTGCTGCTGCA 120
Db      61  CTGGGCAAGGCACAATGAACCGGGAGTCCCTTTTAGGCACTTGTGTGCTGCTGCA 120
Qy      121  CTGGGCTCTCTCCAGAGGCACTCAAGAGAAAGTGTGTGTGGCAAAAAGGGAT 180
Db      121  CTGGGCTCTCTCCAGAGGCACTCAAGAGAAAGTGTGTGTGGCAAAAAGGGAT 180
Qy      181  ACAGTGAATCTGACCTGTACAGTCTCCAGAGAAAGCATACATTCCTGGAAGAAC 240
Db      181  ACAGTGAATCTGACCTGTACAGTCTCCAGAGAAAGCATACATTCCTGGAAGAAC 240
Qy      241  TCCAAACAGATAAAGATTCTGGGAAATCAGGGCTCTCTTAACTAAAGGTCCATCCAG 300
Db      241  TCCAAACAGATAAAGATTCTGGGAAATCAGGGCTCTCTTAACTAAAGGTCCATCCAG 300
Qy      301  CTGAATGATCGCGCTGACTCAAGAGAAAGCTTTGGGACCAAGAAACTTCCCTGATC 360
Db      301  CTGAATGATCGCGCTGACTCAAGAGAAAGCTTTGGGACCAAGAAACTTCCCTGATC 360
Qy      361  ATCAAGATCTTAAAGATAGAAAGCTCAGATTAATCTGTGTGAAGTGAAGACAGAG 420
Db      361  ATCAAGATCTTAAAGATAGAAAGCTCAGATTAATCTGTGTGAAGTGAAGACAGAG 420
Qy      421  GAGAGGTGCAATTGCTAGTGTGAGATTGACTGCCAATCTGACACCCAGCTGCTCAG 480
Db      421  GAGAGGTGCAATTGCTAGTGTGAGATTGACTGCCAATCTGACACCCAGCTGCTCAG 480
Qy      481  GGGCAGAGCTGACCTTGAACCTTGAAGAGCCCTCTGTAGTACCCCTCAGTGAATGT 540
Db      481  GGGCAGAGCTGACCTTGAACCTTGAAGAGCCCTCTGTAGTACCCCTCAGTGAATGT 540
Qy      541  AGAGTCCAAAGGGGTAAACATACAGGGGGGAAAGACCTCTCCGTGTCTCAGCTGAG 600
Db      541  AGAGTCCAAAGGGGTAAACATACAGGGGGGAAAGACCTCTCCGTGTCTCAGCTGAG 600
Qy      601  CTCAGAGTATGGGCACTGAGCATGCACTGTGTGAAGAACCAAGAAAGTGAAGTTC 660
Db      601  CTCAGAGTATGGGCACTGAGCATGCACTGTGTGAAGAACCAAGAAAGTGAAGTTC 660
Qy      661  AAAATAGACATGCTGCTGCTAGCTTTCACTGAGCTGACCATGCTTCACTTCCG 720
Db      661  AAAATAGACATGCTGCTGCTAGCTTTCACTGAGCTGACCATGCTTCACTTCCG 720
Qy      721  CCATCTGATGAGCAGTTGAAATCTGAACTGCTCTGTGTGTGCTGCTGAAATTAATTC 780
Db      721  CCATCTGATGAGCAGTTGAAATCTGAACTGCTCTGTGTGTGCTGCTGAAATTAATTC 780
Qy      781  TATCCCAAGAGGCGCAAAAGTCACTGGAAGGTGATTAACGCTTCAATGGGTAACTCC 840
Db      781  TATCCCAAGAGGCGCAAAAGTCACTGGAAGGTGATTAACGCTTCAATGGGTAACTCC 840
Qy      841  CAGAGAGTGTCAAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAG 900

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 03:40:26 / Search time 3662.81 Seconds  
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Perfect score: 1149  
Sequence: 1 CAAGCCAGAGCCCTGCCAT.....TCACCCCTCTCTCTCTCTT 1149

Scoring table: IDENTITY NUC  
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Searched: 32822875 seqs, 18219865908 residues  
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Post-processing: Minimum Match 0%  
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2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_g861.\*  
9: gb\_g862.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	655.4	57.0	932	5 BX438745	BX438745 BX438745
2	645.4	56.2	783	6 CD609192	CD609192 56069931J
3	642.8	55.9	816	4 BX1838409	BX1838409 60308373
4	633.4	55.1	801	4 BX1822118	BX1822118 603039813
5	632	55.0	822	5 BX457159	BX457159 BX457159
6	630.2	54.8	840	4 BX1838693	BX1838693 603087279
7	623.4	54.3	791	4 BX1819727	BX1819727 603041415
8	586.6	51.1	713	5 BX437619	BX437619 BX437619
9	553.4	48.2	723	4 BX1915265	BX1915265 603184313
10	551.4	48.0	679	6 CD609191	CD609191 56069931H
11	549	47.8	732	1 AUI41298	AUI41298 AUI41298
12	533.6	46.5	750	7 CO246446	CO246446 AGENCOURT
13	533.4	46.4	710	6 CF125444	CF125444 UI-HF-EL0
14	528.8	46.0	694	6 CB052686	CB052686 NISC_g109
15	525.6	45.7	803	7 CO249540	CO249540 AGENCOURT
16	502.4	43.7	748	5 BX378811	BX378811 BX378811
17	497.8	43.3	821	7 CO245985	CO245985 AGENCOURT
18	474.4	41.3	616	6 CP125140	CP125140 UI-HF-EL0
19	453.6	39.5	809	7 CO248894	CO248894 AGENCOURT
20	453	39.4	640	5 BU679704	BU679704 UI-CF-BC1
21	452.6	39.4	751	7 CO248544	CO248544 AGENCOURT
22	451.8	39.3	641	5 BQ062789	BQ062789 AGENCOURT
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24	451.4	39.3	555	4 BT111498	BT111498 id97ell.x

c	25	451.4	39.3	583	5 BU682271	BU682271 UI-CF-BC1
c	26	451.4	39.3	593	6 CB985747	CB985747 AGENCOURT
c	27	451.4	39.3	611	6 CA413070	CA413070 UI-H-EZ0
c	28	451.4	39.3	620	4 BM511892	BM511892 iJ75d09.x
c	29	451.4	39.3	643	6 CA412343	CA412343 UI-H-EZ0
c	30	451.4	39.3	648	5 BM974791	BM974791 UI-CF-BC1
c	31	451.4	39.3	692	6 CA447921	CA447921 UI-H-EI0
c	32	451.4	39.3	712	5 BU616742	BU616742 UI-H-DF0
c	33	451.4	39.3	731	5 BQ181514	BQ181514 UI-H-EU0
c	34	451.4	39.3	776	5 BQ008671	BQ008671 UI-H-EI0
c	35	451.4	39.3	798	5 BQ008761	BQ008761 UI-H-EI0
c	36	450.6	39.2	536	6 CB958453	CB958453 AGENCOURT
c	37	450.4	39.2	566	4 B1765045	B1765045 603051192
c	38	450.4	39.2	597	6 CB958067	CB958067 AGENCOURT
c	39	450.4	39.2	603	6 CB957083	CB957083 AGENCOURT
c	40	450.4	39.2	606	6 CB957735	CB957735 AGENCOURT
c	41	450.4	39.2	643	5 BQ712156	BQ712156 AGENCOURT
c	42	450.4	39.2	927	5 BQ706352	BQ706352 AGENCOURT
c	43	450.2	39.2	714	6 CA411822	CA411822 UI-H-EZ0
c	44	450	39.2	521	6 CB956541	CB956541 AGENCOURT
c	45	450	39.2	527	1 AU708624	AU708624 AU708624

## ALIGNMENTS

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LOCUS BX438745 932 bp mRNA linear EST 05-MAY-2004  
DEFINITION BX438745 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DB002YG01  
5-PRIME, mRNA sequence.  
ACCESSION BX438745  
VERSION BX438745.2 GI:47035651  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 932)  
L1.W.B., Gruber,C., Jesse,J., and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
COMMENT On May 15, 2003 this sequence version replaced gi:30787731.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.  
This sequence belongs to sequence cluster 6485.x  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?cs=CS0DB002AD01Q1&c=6485.r.  
Location/Qualifiers  
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."  
ORIGIN  
Query Match 57.0%; Score 655.4; DB 5; Length 932;  
Best Local Similarity 98.1%; Pred. No. 1.0e-117;  
Matches 674; Conservative 0; Mismatches 11; Indels 2; Gaps 1;



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QY 11 GCCCTGCAATTTCTGTGGGCTCAGAGTCCCTACTGCTC--AGCCCTTCTCTCCCTGGCAA 68
DB 113 GCCCTGCAATTTCTGTGGGCTCAGAGTCCCTACTGCTCAGAGCCCTGCTCCCTGGCAA 172
QY 69 GGGCCCAATGAAACCGGGGAGTCCCTTTTAAAGCACTTCTGTGTCTGCACTGGGCT 128
DB 173 GGGCCCAATGAAACCGGGGAGTCCCTTTTAAAGCACTTCTGTGTCTGCACTGGGCT 232
QY 129 CTTCCGACAGCCCACTAGAGGAAAGAAAGTGTGTCTGGGCAAAAAGGGGATACAGTGA 188
DB 233 CTTCCGACAGCCCACTAGAGGAAAGAAAGTGTGTCTGGGCAAAAAGGGGATACAGTGA 292
QY 189 ACTGACCTGTACAGCTTCCGAGAAAGAGATCAATTCACATGAAAACTCCAAACA 248
DB 293 ACTGACCTGTACAGCTTCCGAGAAAGAGATCAATTCACATGAAAACTCCAAACA 352
QY 249 GATTAATATTTCTGGGAAATCAGGGCTCTTCTTAACTAAAGGTTCATCCAGCTGAATGA 308
DB 353 GATTAATATTTCTGGGAAATCAGGGCTCTTCTTAACTAAAGGTTCATCCAGCTGAATGA 412
QY 309 TCGGCTGACTCAAGAAAGAGCCCTTGGGACCAAGAAACTCCCGTGAATCAAGAA 368
DB 413 TCGGCTGACTCAAGAAAGAGCCCTTGGGACCAAGAAACTTTCCTGATCATCAAGAA 472
QY 369 TCTTAAGATGAAAGACTCAAGTACTTACATCTGTGAAGTGGAGACCAAGAGAGAGT 428
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QY 489 CTTGACCTGTGACTTGGAGAGCCCTTGGAGTGAAGCCCTCAGTGAATGTGGAATCC 548
DB 593 CTTGACCTGTGACTTGGAGAGCCCTTGGAGTGAAGCCCTCAGTGAATGTGGAATCC 652
QY 549 AAGGGGTAAACATACAGGGGGGAGAGACCTCTCCGTGTCTGAGTGGAGCTCCAGA 608
DB 653 AAGGGGTAAACATACAGGGGGGAGAGACCTCTCCGTGTCTGAGTGGAGCTCCAGA 712
QY 609 TAGTGGCACTGCACTGCACTGTCTTGCAGAACCAAGAGGTGAATCAAAATAGA 668
DB 713 TAGTGGCACTGCACTGCACTGTCTTGCAGAACCAAGAGGTGAATCAAAATAGA 772
QY 669 CATGTGTGTGTGCTTCACTGTGGC 695
DB 773 CATGTGTGTGTGCTTCACTGTGGC 799

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RESULT 2
LOCUS CD609192 783 bp mRNA linear EST 12-JAN-2004
DEFINITION S606993J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD609192
VERSION CD609192.1 GI:40257455
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL 1 (bases 1 to 783)
FUG.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
1..783

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FEATURES
Source

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/organism="Homo sapiens"
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Query Match 56.2%; Score 645.4; DB 6; Length 783;
Best Local Similarity 98.1%; Pred. No. 1,1e-168;
Matches 664; Conservative 0; Mismatches 11; Indels 2; Gaps 1;

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ORIGIN
QY 21 TTCTGTGGCTCAGGTCCTTACTG--CTCAGCCCTTCTCTCTCGCAAGGCCACATG 78
DB 783 TTCTGTGGCTCAGGTCCTTACTGCTCAGGCCCTTCTCTCGCAAGGCCACATG 724
QY 79 AACCGGGAGTCCCTTTAGGCACTTGTGTGTGTGCACTGGGCTCCCTCCAGCA 138
DB 723 AACCGGGAGTCCCTTTAGGCACTTGTGTGTGTGCACTGGGCTCCCTCCAGCA 664
QY 139 GCCACTCAGGGAAGAAAGTGTGTGTGGCAAAAAGGGATCAAGTGAATGACCTGT 198
DB 663 GCCACTCAGGGAAGAAAGTGTGTGTGGCAAAAAGGGATCAAGTGAATGACCTGT 604
QY 199 ACACTTCCCAAGAAAGAGCATACATTCACCTGAAAACTCCAAACGATPAAGATT 258
DB 603 ACACTTCCCAAGAAAGAGCATACATTCACCTGAAAACTCCAAACGATPAAGATT 544
QY 259 CTGGGAATAGGGCTCTCTTAACTAAAGGTCAATCCAGCTGAATGATCGGCTGAC 318
DB 543 CTGGGAATAGGGCTCTCTTAACTAAAGGTCAATCCAGCTGAATGATCGGCTGAC 484
QY 319 TCAAGAAAGAGCTTGTGGACCAAGAAACTTCCCTGATCATCAAGATCTTAAGATA 378
DB 483 TCAAGAAAGAGCTTGTGGACCAAGAAACTTCCCTGATCATCAAGATCTTAAGATA 424
QY 379 GAAGACTCAGATACCTTACATCTGTGAAGTGAAGACCAAGAGAGGTGCAATTGCTA 438
DB 423 GAAGACTCAGATACCTTACATCTGTGAAGTGAAGACCAAGAGAGGTGCAATTGCTA 364
QY 439 GTTGTGGATTTGACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 498
DB 363 GTTGTGGATTTGACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 304
QY 499 ACCTTGAGAGAGCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 558
DB 303 ACCTTGAGAGAGCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 244
QY 559 AACATACAGGGGGGAGAAACCTCTCCGTGTCTCAGCTGAGCTCCAGATAGTGACACC 618
DB 243 AACATACAGGGGGGAGAAACCTCTCCGTGTCTCAGCTGAGCTCCAGATAGTGACACC 184
QY 619 TGAACATGCACTCTCTTGCAGAACCAAGAAAGTGAAGTCAAAATAGCATCTGTGTG 678
DB 183 TGAACATGCACTCTCTTGCAGAACCAAGAAAGTGAAGTCAAAATAGCATCTGTGTG 124
QY 679 CTAGCTTCACTGTGGC 695
DB 123 CTAGCTTCACTGTGGC 107

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RESULT 3
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DEFINITION 603083373F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222323 5',
ACCESSION BI838409
VERSION BI838409.1 GI:15949959
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL 1 (bases 1 to 816)

```



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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 00:11:21 ; Search time 553.457 Seconds  
(without alignments)  
10898.026 Million cell updates/sec

Title: US-08-485-163-6  
Perfect score: 1149  
Sequence: 1 CAAGCCGAGGCGCTGCAT.....TCACCCCGCTCTCTCTT 1149

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues  
Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq 23Sep04:\*

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10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1149	100.0	1149	2	AAQ28090
2	1149	100.0	1149	3	AAZ98857
3	1149	100.0	1149	4	AAAF56397
4	1149	100.0	1149	4	AAAF77831
5	1149	100.0	1149	10	ABSS5722
6	1149	100.0	1149	11	ADMI18323
7	1147.4	99.8	1149	2	AAQ27832
8	1147	99.8	1149	2	AAQ27832
9	1107	96.3	11228	10	ACH00964
10	1062	92.4	3273	10	ACH00965
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12	696.8	60.6	2482	2	AAQ28089
13	696.8	60.6	2482	3	AAZ98856
14	696.8	60.6	2482	4	AAAF56396
15	696.8	60.6	2482	4	AAAF77830
16	696.8	60.6	2482	10	ABSS5721
17	696.8	60.6	2482	11	ADMI18321
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19	687	59.8	1415	2	AAQ38761
20	687	59.8	1421	2	AAQ38760
21	687	59.8	1448	2	AAQ38759

22	687	59.8	1742	3	AAA35205
23	687	59.8	1742	3	AAAF21327
24	687	59.8	1742	4	AAI65462
25	687	59.8	1742	10	ABZ97021
26	687	59.8	1742	11	AD131687
27	687	59.8	1742	11	ABD20870
28	687	59.8	1796	2	AAQ28088
29	687	59.8	1796	2	AAQ57750
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31	687	59.8	1796	4	AAAF56395
32	687	59.8	1796	4	AAAF77829
33	687	59.8	1796	10	ABSS5720
34	687	59.8	1806	2	AAQ27830
35	687	59.8	6019	3	AAA35208
36	687	59.8	6019	3	AAAF21330
37	687	59.8	6019	10	ABZ97024
38	687	59.8	6019	11	ABD20873
39	685.4	59.7	1742	1	AAAB80512
40	685.4	59.7	1742	1	AAAB90619
41	685.4	59.7	1742	2	AAZ20695
42	685.4	59.7	1742	2	AAAS9352
43	685.4	59.7	2465	2	AAQ38758
44	683.8	59.5	1273	1	AAAB90763
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## ALIGNMENTS

RESULT 1	AAQ28090	standard; DNA; 1149 BP.
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DT	25-MAR-2003	(revised)
DT	06-FEB-1993	(first entry)
XX		
DE	Encodes CD4-IgG2 chimeric light chain.	
XX		
KW	homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery;	
KW	chimeric; increased serum half life; HIV infection; AIDe; ss.	
XX		
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	CDS	/tag= a*
FT		/label= CD4 domain
FT	CDS	/tag= b*
FT		/label= Ckappa domain
XX		
XX	W09213947-A1.	
XX	20-AUG-1992.	
XX	10-FEB-1992;	92WO-US001143.
XX	08-FEB-1991;	91US-00653684.
XX	(PROG-) PROGENICS PHARM INC.	
XX	Beaudry GA, Maddon PJ;	
XX	WPI; 1992-300034/36.	
XX	P-PSDB; AAR26784.	
XX	CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for	
XX	treatment, prevention and diagnosis of HIV infection.	



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OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 09:02:41 ; Search time 620.542 Seconds  
(without alignments)  
10639.123 Million cell updates/sec

Title: US-08-485-163-6  
Perfect score: 1149  
Sequence: 1 CAAGCCGAGAGCCCTGCGCAT.....TCACCCCTCTCTCTCTT 1149

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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- 19: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 20: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1149	100.0	1149	9	US-09-766-995-5
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4	1062	92.4	3273	16	US-10-397-569-7
5	996.8	60.6	2482	8	US-08-485-163-4
6	996.8	60.6	2482	9	US-09-766-995-3
7	687	59.8	1742	14	US-10-151-274-7
8	687	59.8	1742	16	US-10-641-643-1013
9	687	59.8	1796	8	US-08-485-163-2
10	687	59.8	1796	9	US-09-766-995-1
11	685.4	59.7	1742	11	US-09-891-119A-8
12	683.8	59.5	1273	11	US-09-891-119A-1

13	683.8	59.5	1416	15	US-10-157-408-2	Sequence 2, Appli
14 <td>683.8<th>59.5</th><th>1416</th><th>18</th><th>US-10-097-044A-2</th><th>Sequence 2, Appli</th></td>	683.8 <th>59.5</th> <th>1416</th> <th>18</th> <th>US-10-097-044A-2</th> <th>Sequence 2, Appli</th>	59.5	1416	18	US-10-097-044A-2	Sequence 2, Appli
15 <td>683.8<th>59.5</th><th>1416</th><th>18</th><th>US-10-769-247-2</th><th>Sequence 2, Appli</th></td>	683.8 <th>59.5</th> <th>1416</th> <th>18</th> <th>US-10-769-247-2</th> <th>Sequence 2, Appli</th>	59.5	1416	18	US-10-769-247-2	Sequence 2, Appli
16 <td>660.4<th>57.5</th><th>1745</th><th>15</th><th>US-10-024-329-1</th><th>Sequence 1, Appli</th></td>	660.4 <th>57.5</th> <th>1745</th> <th>15</th> <th>US-10-024-329-1</th> <th>Sequence 1, Appli</th>	57.5	1745	15	US-10-024-329-1	Sequence 1, Appli
17 <td>655.4<th>57.0</th><th>1304</th><th>15</th><th>US-09-939-537-28</th><th>Sequence 28, Appli</th></td>	655.4 <th>57.0</th> <th>1304</th> <th>15</th> <th>US-09-939-537-28</th> <th>Sequence 28, Appli</th>	57.0	1304	15	US-09-939-537-28	Sequence 28, Appli
18 <td>655.4<th>57.0</th><th>3084</th><th>15</th><th>US-10-207-655-169</th><th>Sequence 169, App</th></td>	655.4 <th>57.0</th> <th>3084</th> <th>15</th> <th>US-10-207-655-169</th> <th>Sequence 169, App</th>	57.0	3084	15	US-10-207-655-169	Sequence 169, App
19 <td>652.4<th>56.8</th><th>719</th><th>10</th><th>US-09-939-537-30</th><th>Sequence 10, Appli</th></td>	652.4 <th>56.8</th> <th>719</th> <th>10</th> <th>US-09-939-537-30</th> <th>Sequence 10, Appli</th>	56.8	719	10	US-09-939-537-30	Sequence 10, Appli
20 <td>612<th>53.3</th><th>617</th><th>18</th><th>US-10-493-676-7</th><th>Sequence 7, Appli</th></td>	612 <th>53.3</th> <th>617</th> <th>18</th> <th>US-10-493-676-7</th> <th>Sequence 7, Appli</th>	53.3	617	18	US-10-493-676-7	Sequence 7, Appli
21 <td>612<th>53.3</th><th>1377</th><th>14</th><th>US-10-103-597A-38</th><th>Sequence 38, Appli</th></td>	612 <th>53.3</th> <th>1377</th> <th>14</th> <th>US-10-103-597A-38</th> <th>Sequence 38, Appli</th>	53.3	1377	14	US-10-103-597A-38	Sequence 38, Appli
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24 <td>610.4<th>53.1</th><th>1389</th><th>11</th><th>US-09-939-537-2</th><th>Sequence 2, Appli</th></td>	610.4 <th>53.1</th> <th>1389</th> <th>11</th> <th>US-09-939-537-2</th> <th>Sequence 2, Appli</th>	53.1	1389	11	US-09-939-537-2	Sequence 2, Appli
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26 <td>610.4<th>53.1</th><th>1599</th><th>10</th><th>US-09-939-537-3</th><th>Sequence 3, Appli</th></td>	610.4 <th>53.1</th> <th>1599</th> <th>10</th> <th>US-09-939-537-3</th> <th>Sequence 3, Appli</th>	53.1	1599	10	US-09-939-537-3	Sequence 3, Appli
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28 <td>610.4<th>53.1</th><th>1728</th><th>10</th><th>US-09-939-537-1</th><th>Sequence 1, Appli</th></td>	610.4 <th>53.1</th> <th>1728</th> <th>10</th> <th>US-09-939-537-1</th> <th>Sequence 1, Appli</th>	53.1	1728	10	US-09-939-537-1	Sequence 1, Appli
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33 <td>571.4<th>49.7</th><th>573</th><th>15</th><th>US-10-024-329-31</th><th>Sequence 31, Appli</th></td>	571.4 <th>49.7</th> <th>573</th> <th>15</th> <th>US-10-024-329-31</th> <th>Sequence 31, Appli</th>	49.7	573	15	US-10-024-329-31	Sequence 31, Appli
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#### ALIGNMENTS

RESULT 1  
US-08-485-163-6  
; Sequence 6, Application US/08485163  
; Publication No. US20020098191A1  
; GENERAL INFORMATION:  
; APPLICANT: Beaudry, Gary A.  
; APPLICANT: Maddon, Paul J.  
; TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,163  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 37690-II-1-PCT-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 1149 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: cdna  
ORIGINAL SOURCE: cdna  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-08-485-163-6

Query Match 100.0%; Score 1149; DB 8; Length 1149;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CAAGCCAGAGCCCTGCAATTTCTGTGGGCTCAGGTCCCTACTGAGCCCTTCTCC 60  
QY 61 CTCGGCAAGGCGCACATGAACCGGGGAGTCCCTTTAGGCACTTGCTTGCTGCA 120  
DB 61 CTCGGCAAGGCGCACATGAACCGGGGAGTCCCTTTAGGCACTTGCTTGCTGCA 120  
QY 121 CTGGCGCTCTCCAGAGCCCACTCAAGGAAAGAAAGTGTGCTGGGCAAAAAAGG 180  
DB 121 CTGGCGCTCTCCAGAGCCCACTCAAGGAAAGAAAGTGTGCTGGGCAAAAAAGG 180  
QY 181 ACAGTGAATGACCTGTACAGCTTCCAGAGAAAGACATACATTCCTGAGAAAAAC 240  
DB 181 ACAGTGAATGACCTGTACAGCTTCCAGAGAAAGACATACATTCCTGAGAAAAAC 240  
QY 241 TCACAACAGATAAAGATTCTGGGAAATCAAGGCTCTTCTTAACTAAAGTCCATCC 300  
DB 241 TCACAACAGATAAAGATTCTGGGAAATCAAGGCTCTTCTTAACTAAAGTCCATCC 300  
QY 301 CTGAATGATGCGCGCTGACTCAAGAAAGACCTTTGGGACCAAGAACTTCCCTGATC 360  
DB 301 CTGAATGATGCGCGCTGACTCAAGAAAGACCTTTGGGACCAAGAACTTCCCTGATC 360  
QY 361 ATCAAGATCTTAAGATAGAAAGCTCAGATCTACATCTGTGAAGTGAAGACAGAG 420  
DB 361 ATCAAGATCTTAAGATAGAAAGCTCAGATCTACATCTGTGAAGTGAAGACAGAG 420  
QY 421 GAGAGGTGCAATGCTAGTGTGGAATGACTGCACTGCACTGCACTGCTTCCAG 480  
DB 421 GAGAGGTGCAATGCTAGTGTGGAATGACTGCACTGCACTGCACTGCTTCCAG 480  
QY 481 GGGGAGGCTGACCTGCACTTGTGGAAGAGCCCTGCTGATAGCCCTCAGTCAATGT 540  
DB 481 GGGGAGGCTGACCTGCACTTGTGGAAGAGCCCTGCTGATAGCCCTCAGTCAATGT 540  
QY 541 AGAGTCCAAGGGGTAAACATACAGGGGGGAAAGCCCTCTCGTGTCTCAGCTGAG 600  
DB 541 AGAGTCCAAGGGGTAAACATACAGGGGGGAAAGCCCTCTCGTGTCTCAGCTGAG 600  
QY 601 CTCAGAGTATGCACTGCACTGCACTGCTTCTTGGAGAACAGAAAGTGAAGTTC 660  
DB 601 CTCAGAGTATGCACTGCACTGCACTGCTTCTTGGAGAACAGAAAGTGAAGTTC 660  
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DB 661 AAAATTAAGCATCTGTGTGCTAGCTTTCACTGTGCTGCACTGTCTTCAATTTCCG 720  
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QY 841 CAGAGAGTGTCAAG 900  
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QY 1081 TCACAAG 1140  
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QY 1141 CTCCTCCTT 1149  
DB 1141 CTCCTCCTT 1149

RESULT 2  
US-09-766-995-5  
Sequence 5, Application US/09766995  
Patent No. US20020052481A1  
GENERAL INFORMATION:  
APPLICANT: Graham P. Allaway et al.  
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-1G52 IMMUNOCONJ  
FILE REFERENCE: 2048/41215-CB/JPW/SHS  
CURRENT FILING DATE: 2001-01-22  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5  
LENGTH: 1149  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-766-995-5

Query Match 100.0%; Score 1149; DB 9; Length 1149;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CAAGCCAGAGCCCTGCAATTTCTGTGGGCTCAGGTCCCTACTGAGCCCTTCTCC 60  
QY 61 CTCGGCAAGGCGCACATGAACCGGGGAGTCCCTTTAGGCACTTGCTTGCTGCA 120  
DB 61 CTCGGCAAGGCGCACATGAACCGGGGAGTCCCTTTAGGCACTTGCTTGCTGCA 120  
QY 121 CTGGCGCTCTCCAGAGCCCACTCAAGGAAAGAAAGTGTGCTGGGCAAAAAAGG 180  
DB 121 CTGGCGCTCTCCAGAGCCCACTCAAGGAAAGAAAGTGTGCTGGGCAAAAAAGG 180  
QY 181 ACAGTGAATGACCTGTACAGCTTCCAGAGAAAGACATACATTCCTGAGAAAAAC 240  
DB 181 ACAGTGAATGACCTGTACAGCTTCCAGAGAAAGACATACATTCCTGAGAAAAAC 240  
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DB 241 TCACAACAGATAAAGATTCTGGGAAATCAAGGCTCTTCTTAACTAAAGTCCATCC 300  
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QY 361 ATCAAGATCTTAAGATAGAAAGCTCAGATCTTCACTGTGAAGTGAAGAGAGAG 420  
DB 361 ATCAAGATCTTAAGATAGAAAGCTCAGATCTTCACTGTGAAGTGAAGAGAGAG 420

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## OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 03:49:56 ; Search time 98.0969 seconds  
(without alignments)  
8325.401 Million cell updates/sec

Title: US-08-485-163-6  
Perfect score: 1149

Sequence: 1 CAGGCCGAGGCCCTGCCAT.....TCACCCCTCTCTCTCTT 1149

Scoring table: IDENTITY\_NUC  
Gap 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

1: Issued Patents NA: \*  
2: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
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6: /cgn2\_6/ptodata/1/ina/PTCTUS\_COMB.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1149	100.0	1149	3	US-08-477-460B-5
2	1149	100.0	1149	3	US-08-379-516-5
3	1149	100.0	1149	3	US-09-329-916-5
4	1149	100.0	1149	3	US-08-485-372A-5
5	1149	100.0	1149	3	US-09-409-006A-5
6	1149	100.0	1149	4	US-08-484-681-5
7	1149	100.0	1149	4	US-09-766-995-5
8	1149	100.0	1149	5	PCT-US93-07422-5
9	696.8	60.6	2482	3	US-08-477-460B-3
10	696.8	60.6	2482	3	US-08-379-516-3
11	696.8	60.6	2482	3	US-09-329-916-3
12	696.8	60.6	2482	3	US-08-485-372A-3
13	696.8	60.6	2482	3	US-09-409-006A-3
14	696.8	60.6	2482	4	US-08-484-681-3
15	696.8	60.6	2482	4	US-09-766-995-3
16	696.8	60.6	2482	5	PCT-US93-07422-3
17	687	59.8	1415	5	PCT-US92-08090-4
18	687	59.8	1421	5	PCT-US92-08090-3
19	687	59.8	1448	5	PCT-US92-08090-2
20	687	59.8	1742	4	US-09-517-605-7
21	687	59.8	1742	4	US-09-023-655-1013
22	687	59.8	1796	3	US-08-477-460B-1
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24	687	59.8	1796	3	US-09-329-916-1
25	687	59.8	1796	3	US-08-485-372A-1
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27	687	59.8	1796	4	US-08-484-681-1

28	687	59.8	1796	4	US-09-766-995-1	Sequence 1, Appli
29	687	59.8	1796	5	PCT-US93-07422-1	Sequence 1, Appli
30	687	59.8	2465	5	PCT-US92-08090-1	Sequence 1, Appli
31	685.4	59.7	1742	3	US-08-466-368-3	Sequence 1, Appli
32	685.4	59.7	1742	4	US-08-470-998-1	Sequence 2, Appli
33	685.4	59.7	1742	4	US-08-328-500-8	Sequence 8, Appli
34	683.8	59.5	1273	3	US-08-466-368-1	Sequence 1, Appli
35	683.8	59.5	1273	3	US-08-328-500-1	Sequence 1, Appli
36	683.8	59.5	1416	1	US-08-226-311-2	Sequence 2, Appli
37	683.8	59.5	1416	3	US-08-457-918-2	Sequence 2, Appli
38	683.8	59.5	1416	3	US-10-157-408-2	Sequence 2, Appli
39	664	57.0	1213	6	5223418-1	Patent No. 5223418
40	655.4	57.0	1304	2	US-08-284-391B-28	Sequence 28, Appli
41	655.4	57.0	1304	3	US-09-218-950-28	Sequence 28, Appli
42	655.4	57.0	1304	4	US-08-394-388A-28	Sequence 28, Appli
43	655.4	57.0	2589	4	US-08-472-888A-5	Sequence 5, Appli
44	652.4	56.8	719	2	US-08-284-391B-30	Sequence 30, Appli
45	652.4	56.8	719	3	US-09-218-950-30	Sequence 30, Appli

## ALIGNMENTS

RESULT 1  
US-08-477-460B-5  
Sequence 5, Application US/08477460B  
Patent No. 6034223  
GENERAL INFORMATION:  
APPLICANT: Progenics Pharmaceuticals, Inc.  
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED  
TITLE OF INVENTION: CD4-GMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,460B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/927,931  
FILING DATE: 07-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 977-9809  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1149 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: cdna  
ORIGINAL SOURCE:  
ORGANISM: homo sapien  
CELL TYPE: lymphocyte  
US-08-477-460B-5  
Query Match 100.0%; Score 1149; DB 3; Length 1149;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGCCAGAGCCCTGCAATTTCTGTGGGCTCAGGTCCCTACTGCTCAGCCCTTCTCC 60  
Db 1 CAAGCCAGAGCCCTGCAATTTCTGTGGGCTCAGGTCCCTACTGCTCAGCCCTTCTCC 60

QY 61 CTGGGCAAGGCGCAATGAAACCGGGAGTCCCTTTTAAAGCACTTGTCTGTGCTGCA 120  
Db 61 CTGGGCAAGGCGCAATGAAACCGGGAGTCCCTTTTAAAGCACTTGTCTGTGCTGCA 120

QY 121 CTGGGCGCTCCCTCCAGAGCCACTCAAGGAAAGAAAGTGTGCTGGGCAAAAAAGGGAT 180  
Db 121 CTGGGCGCTCCCTCCAGAGCCACTCAAGGAAAGAAAGTGTGCTGGGCAAAAAAGGGAT 180

QY 181 ACAATGGAATCTGACTGTACTGCTCCAGAAAGAGCATATCAATTCCTACTGAAAAAC 240  
Db 181 ACAATGGAATCTGACTGTACTGCTCCAGAAAGAGCATATTCCTACTGAAAAAC 240

QY 241 TCCAACCAAGATTAAGATTCTGGAAATCAAGGGCTCTTTTAACTAAAGTCCATCCAG 300  
Db 241 TCCAACCAAGATTAAGATTCTGGAAATCAAGGGCTCTTTTAACTAAAGTCCATCCAG 300

QY 301 CTGAATATGCGCGTGACTCAAGAAAGCCTTTGGGACCAAGAACTTCCCTGATC 360  
Db 301 CTGAATATGCGCGTGACTCAAGAAAGCCTTTGGGACCAAGAACTTCCCTGATC 360

QY 361 ATCAAGAATCTTAAGATTAAGAACTCAGATCTACTTACATCTGTGAAGTGAAGACCAAG 420  
Db 361 ATCAAGAATCTTAAGATTAAGAACTCAGATCTACTTACATCTGTGAAGTGAAGACCAAG 420

QY 421 GAGGAGGTGCAATGCTAGTGTGGAATTGACTGCCAATCTGACACCCACTGCTTCA 480  
Db 421 GAGGAGGTGCAATGCTAGTGTGGAATTGACTGCCAATCTGACACCCACTGCTTCA 480

QY 481 GGGGAGAGCCCTGACCTTGAAGAGCCCTTGTGAGTGTAGCCCTCTGATGCAATGT 540  
Db 481 GGGGAGAGCCCTGACCTTGAAGAGCCCTTGTGAGTGTAGCCCTCTGATGCAATGT 540

QY 541 AGGAGTCCAAAGGGGTAAATAATCATACAGGGGGGAAAGACCTCTCGTGTCTCAGTGA 600  
Db 541 AGGAGTCCAAAGGGGTAAATAATCATACAGGGGGGAAAGACCTCTCGTGTCTCAGTGA 600

QY 601 CTCAGAGTATGTCACCTGCACTGCACTGTCTTGCAGAACCAAGAAAGTGAAGTTC 660  
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QY 661 AAAATAGCATCTGTGTGCTAGCTTTCACTGTGCTGCACTGTCTTCACTTCCG 720  
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QY 721 CCATCTGATGAGCAGTTGAATCTGAACTGCTCTGTGTGTGCTGCTGAATPACTTC 780  
Db 721 CCATCTGATGAGCAGTTGAATCTGAACTGCTCTGTGTGTGCTGCTGAATPACTTC 780

QY 781 TATCCAGAGAGGCCAAAGTACAGTGAAGGTGATTAAGCCCTTCAATCGGATPACTTC 840  
Db 781 TATCCAGAGAGGCCAAAGTACAGTGAAGGTGATTAAGCCCTTCAATCGGATPACTTC 840

QY 841 CAGAGAGTGTCAAGAGCAGAGACAGCAAGACAGCACTACAGCTTCAAGCACTTCG 900  
Db 841 CAGAGAGTGTCAAGAGCAGAGACAGCAAGACAGCACTACAGCTTCAAGCACTTCG 900

QY 901 ACGGTGAGCAAAAGAGACTAGAGAAACAAGAGTCTACAGCTGCGAAGTCAACCACTAG 960  
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QY 961 GGCCTGAGCTCGCCCTCACAAAGAGCTTCAACAGGGAGAGTGTAGAGGAGAAAGTGC 1020  
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QY 1081 TCACAGAGGAGCTTACCCCTATTGCGGTCTCCAGGCTCATCTTTCACCTCACCCCTC 1140  
Db 1081 TCACAGAGGAGCTTACCCCTATTGCGGTCTCCAGGCTCATCTTTCACCTCACCCCTC 1140

QY 1141 CTCCTCCTT 1149  
Db 1141 CTCCTCCTT 1149

RESULT 2  
US-08-379-516-5  
; Sequence 5, Application US/08379516  
; Patent No. 6083478  
; GENERAL INFORMATION:  
; APPLICANT: Allaway, Graham P.  
; APPLICANT: Maddon, Paul J.  
; TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2  
; FILE REFERENCE: 41215-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/08/379,516  
; CURRENT FILING DATE: 1996-06-10  
; EARLIER APPLICATION NUMBER: PCT/US93/07422  
; EARLIER FILING DATE: 1993-08-06  
; EARLIER APPLICATION NUMBER: 07/927,931  
; EARLIER FILING DATE: 1992-08-07  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 1149  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-08-379-516-5

Query Match 100.0%; Score 1149; DB 3; Length 1149;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGCCAGAGCCCTGCAATTTCTGTGGGCTCAGGTCCCTACTGCTCAGCCCTTCTCC 60  
Db 1 CAAGCCAGAGCCCTGCAATTTCTGTGGGCTCAGGTCCCTACTGCTCAGCCCTTCTCC 60

QY 61 CTGGGCAAGGCGCAATGAAACCGGGAGTCCCTTTTAAAGCACTTGTCTGTGCTGCA 120  
Db 61 CTGGGCAAGGCGCAATGAAACCGGGAGTCCCTTTTAAAGCACTTGTCTGTGCTGCA 120

QY 121 CTGGGCGCTCCCTCCAGAGCCACTCAAGGAAAGAAAGTGTGCTGGGCAAAAAAGGGAT 180  
Db 121 CTGGGCGCTCCCTCCAGAGCCACTCAAGGAAAGAAAGTGTGCTGGGCAAAAAAGGGAT 180

QY 181 ACAATGGAATCTGACTGTACTGCTCCAGAAAGAGCATATCAATTCCTACTGAAAAAC 240  
Db 181 ACAATGGAATCTGACTGTACTGCTCCAGAAAGAGCATATTCCTACTGAAAAAC 240

QY 241 TCCAACCAAGATTAAGATTCTGGAAATCAAGGGCTCTTTTAACTAAAGTCCATCCAG 300  
Db 241 TCCAACCAAGATTAAGATTCTGGAAATCAAGGGCTCTTTTAACTAAAGTCCATCCAG 300

QY 301 CTGAATATGCGCGTGACTCAAGAAAGCCTTTGGGACCAAGAACTTCCCTGATC 360  
Db 301 CTGAATATGCGCGTGACTCAAGAAAGCCTTTGGGACCAAGAACTTCCCTGATC 360

QY 361 ATCAAGAATCTTAAGATTAAGAACTCAGATCTACTTACATCTGTGAAGTGAAGACCAAG 420  
Db 361 ATCAAGAATCTTAAGATTAAGAACTCAGATCTACTTACATCTGTGAAGTGAAGACCAAG 420

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